

clearly present, in the hypervariable domains of env
~~(cf. fig. 6-g and h)~~. As noted for point mutations, env
 gene and orf F also appear as more susceptible to that
 form of genetic variation than the rest of the genome.
 5 The degree of conservation of these repeats must be
 related to their date of occurrence in the analyzed
 sequences : the more degenerated, the more ancient. A
 very recent divergence of LAV_{BRU} and HTLV-3 is suggested
 10 by the extremely low number of mismatched AA between
 their homologous proteins. However, one of the LAV_{BRU}
 repeats (located in the Hyl domain of env, ~~fig. 6-f~~) is
 not present in HTLV-3, indicating that this generation
 of tandem repeats is a rapid source of genetic diver-
 sity. We have found no traces of such a phenomenon, even
 15 when comparing very closely related viruses, such as the
 Mason-Pfizer monkey virus (hereinafter "MPMV") [Sonigo
 et al., 1986], and an immunosuppressive simian virus
 (hereinafter "SRV-1") [Power et al., 1986]. Insertion or
 20 deletion of one copy of a direct repeat have been occa-
 sionally reported in mutant retroviruses [Shimotohno and
 Temin, 1981 ; Darlix, 1986], but the extent to which we
 observe this phenomenon is unprecedented. The molecular
 basis of these duplications is unclear, but could be the
 25 "copy-choice" phenomenon, resulting from the diploidy of
 the retroviral genome [Varmus and Swanstrom, 1984 ;
 Clark and Mak, 1983]. During the synthesis of the first-
 strand of the viral DNA, jumps are known to occur from
 one RNA molecule to another, especially when a break or
 a stable secondary structure is present on the template;
 30 an inaccurate re-initiation on the other RNA template
 could result in the generation (or the elimination) of a
 short direct repeat.

Genetic variability and subsequent antigenic
 35 modifications have often been developed by micro-
 organisms as a means for avoiding the host's immune

90A
8/17/05

90A
8/17/05